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| 121 | CGAGAAAGTTTTGGGAAAGATTCCTCCAGAAATATTTCTTCATTTCTTTTGGAGGACCG | 180 |
| 121 | CGAGAAAGTTTTGGGAAAGATTCCTCCAGAAATATTTCTTCATTTCTTTTGGAGGACCG | 180 |
| 181 | ACTTACTTTTTTTGGTCTCTCTTTATATTAATCTTTTCCCTTTTCCCGCGGTGGGACC | 240 |
| 181 | ACTTACTTTTTTTGGTCTCTCTTTATATTAATCTTTTCCCTTTTCCCGCGGTGGGACC | 240 |
| 241 | GCCGACGCCGTGGAGGAGACCGTAGCTGAAGCTGATTTGTTTATACAGCGCGTGTGCAC | 300 |
| 241 | GCCGACGCCGTGGAGGAGACCGTAGCTGAAGCTGATTTGTTTATACAGCGCGTGTGCAC | 300 |
| 301 | CAAGACGCTTTCTGCCCTGGGGGAGCAACCCCTCCCTCGCTCCCTGGGTCCTACGAGACC | 360 |
| 301 | CAAGACGCTTTCTGCCCTGGGGGAGCAACCCCTCCCTCGCTCCCTGGGTCCTACGAGACC | 360 |
| 361 | TGCACCTTTCAAGAGGTACAGCGGCATCCTGTGGGGCCTGGGCACCGAGGAAGACTGCA | 420 |
| 361 | TGCACCTTTCAAGAGGTACAGCGGCATCCTGTGGGGCCTGGGCACCGAGGAAGACTGCA | 420 |
| 421 | CAGAAACTTTGGCATTTGTGGAAAGGAGAGTGTGGCTCTTCTCCCGAGAGACTTCCCGGACA | 480 |
| 421 | CAGAAACTTTGGCATTTGTGGAAAGGAGAGTGTGGCTCTTCTCCCGAGAGACTTCCCGGACA | 480 |
| 481 | GCCTACTTTGAGACTCGCTCAGCGCACCGTGGGACTCCACGGGCTCACCCCGGACTTG | 540 |
| 481 | GCCTACTTTGAGACTCGCTCAGCGCACCGTGGGACTCCACGGGCTCACCCCGGACTTG | 540 |
| 541 | CACCTTACTTCCCAAAACCCCGGGCATTAAGCCTTGGCTTCCGTGGGACCTCAGCGTGG | 600 |
| 541 | CACCTTACTTCCCAAAACCCCGGGCATTAAGCCTTGGCTTCCGTGGGACCTCAGCGTGG | 600 |
| 601 | TCACGAGTGGCCCCCTGTGGCCCCAGGGAATGTTTCAGGCTTCCCGGAGACTACGA | 660 |
| 601 | TCACGAGTGGCCCCCTGTGGCCCCAGGGAATGTTTCAGGCTTCCCGGAGACTACGA | 660 |
| 661 | CTCCGCTCCCGGTGCAGTCTCTCACCCCTCTGCCGAGTCTCAATATCTGTCTTCGGTGA | 720 |
| 661 | CTCCGCTCCCGGTGCAGTCTCTCACCCCTCTGCCGAGTCTCAATATCTGTCTTCGGTGA | 720 |
| 721 | CTCCTTCGGAGTCCAAACCCACCGCGCGGCTCCCGAGAGTGGCGGCTCTCGGGAA | 780 |
| 721 | CTCCTTCGGAGTCCAAACCCACCGCGCGGCTCCCGAGAGTGGCGGCTCTCGGGAA | 780 |
| 781 | ATGCCCGGTTCTTCTGTGCCCATCCGCTCACCGGATCAACACGACGAGGACCTCCAGTGG | 840 |
| 781 | ATGCCCGGTTCTTCTGTGCCCATCCGCTCACCGGATCAACACGACGAGGACCTCCAGTGG | 840 |
| 841 | CTTGTGCAACCGACCTCATCTCTTCATGGGCGCAGTCCCGAGTGTGCACCACTGGCT | 900 |
| 841 | CTTGTGCAACCGACCTCATCTCTTCATGGGCGCAGTCCCGAGTGTGCACCACTGGCT | 900 |
| 901 | CCACGCCCGGCTGTGCAACCTTAAGAAATTTGGGGAAACCACTTACTCCAACACGAGC | 960 |
| 901 | CCACGCCCGGCTGTGCAACCTTAAGAAATTTGGGGAAACCACTTACTCCAACACGAGC | 960 |
| 961 | ATGAGTGGCTTACAGAGTGGGAGAGAGTGTGGCTTCCACACGCGAACT | 1020 |
| 961 | ATGAGTGGCTTACAGAGTGGGAGAGAGTGTGGCTTCCACACGCGAACT | 1020 |
| 1021 | ACCAGTGGGCTCGGGCTCCCGCCAGCCGAGCGCGGCTTAGAGACCCCGAGAGGAG | 1080 |
| 1021 | ACCAGTGGGCTCGGGCTCGCGCCAGCCCGAGCGCGGCTTAGAGACCCCGAGAGGAG | 1080 |
| 1081 | ACGCTCAACCCAGAGGACAGAGAGAGCGAAGGCTGCGCGGAAACGAATATACTAGC | 1140 |
| 1081 | ACGCTCAACCCAGAGGACAGAGAGAGCGAAGGCTGCGCGGAAACGAATATACTAGC | 1140 |
| 1141 | AGCAGCTAAATGACGGAACCGCGGAGGAGCTGACCGACCGACTCCAGCGGAGACAG | 1200 |
| 1141 | AGCAGCTAAATGACGGAACCGCGGAGGAGCTGACCGGACCGACTCCAGCGGAGACAG | 1200 |
| 1201 | ATCAGTTGGAGGAGAAAACAGACGCTGGAGTCGGAGATGCGCGGAGCTTCCAAAAGTT | 1260 |

APR 25

2281 TTGATGCCCCCTAGATAATCTCATCCGCCACCGGACGTTCTGTTTGAGATGTGAA 2340
 2341 CGTCCCTTCTTGACCTGCTAGGACATCCACTCCCGAGAAATAAGCTGCTCTGATTGG 2400
 2341 CGTCCCTTCTTGACCTGCTAGGACATCCACTCCCGAGAAATAAGCTGCTCTGATTGG 2400
 2401 TATTCTGGGCTGCTAAGGCTCCCGACCCCTGATTAGTATGATGATGATGATGATGATG 2460
 2401 TATTCTGGGCTGCTAAGGCTCCCGACCCCTGATTAGTATGATGATGATGATGATGATG 2460
 2461 CTTTCTGACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
 2521 GCTGCGTGGCTTCTGTTGGGCGCTTCTGATTTTATGCGGAGTCAGGCTGCTGCTGT 2580
 2521 GCTGCGTGGCTTCTGTTGGGCGCTTCTGATTTTATGCGGAGTCAGGCTGCTGCTGT 2580
 2581 GAATGCGCTGCTGCTGGGAGTGATTTATTAACCTGTGAATGATGATGATGATGATGATG 2640
 2581 GAATGCGCTGCTGCTGGGAGTGATTTATTAACCTGTGAATGATGATGATGATGATGATG 2640
 2641 GTGAGCTGGGCTGGGCGACGACCTCATGCGGGGATAAATGTCGGCGCACTTCTCTCG 2700
 2641 GTGAGCTGGGCTGGGCGACGACCTCATGCGGGGATAAATGTCGGCGCACTTCTCTCG 2700
 2701 AAAGCCGTTTCTGCGGTCTCCCGTTCGCGTGCATCCCGGTTTCTTCTCCCTCAACAG 2760
 2701 AAAGCCGTTTCTGCGGTCTCCCGTTCGCGTGCATCCCGGTTTCTTCTCCCTCAACAG 2760
 2761 CAGAGTAGTCAATGGGGGTGACAGACCGAGAAATGGGGGTGACAGTCTCTCGCAAT 2820
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 2821 GCACCTGCTGCGCTGCTGCTCTGCTCTCAGGACCGCTCATGCGCTGAGCGCTGTGTC 2880
 2821 GCACCTGCTGCGCTGCTGCTCTGCTCTCAGGACCGCTCATGCGCTGAGCGCTGTGTC 2880
 2881 TTGCTTTAATGGTCCCCGACCTAATCCCGACGACCTAGGACGCAACTTCTCACACCCC 2940
 2881 TTGCTTTAATGGTCCCCGACCTAATCCCGACGACCTAGGACGCAACTTCTCACACCCC 2940
 2941 TTGCGCCCTCACATCTCTACCTGGAAGGAGTGGGGCTGAGCTATTTTCTCGGA 3000
 2941 TTGCGCCCTCACATCTCTACCTGGAAGGAGTGGGGCTGAGCTATTTTCTCGGA 3000
 3001 CAAGATGCTATGCTGAGTGTTCGGTACCCCAAAACCCACAAATATTTTGGAGCTGG 3060
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 3061 CAGACTCAAGGGGTGGAATCTCATGATTCATGCGCGGATTCGCGCCATCCCTGACCA 3120
 3121 TGGTTTGGCTCTCCACCCCGCTTCCCTGACGCTTCTATCTCATGAGGAGTTCCTT 3180
 3121 TGGTTTGGCTCTCCACCCCGCTTCCCTGACGCTTCTATCTCATGAGGAGTTCCTT 3180
 3181 TATGAGGCAAAATTAATTTTATATGCGGGGTGACACGACCGCCCTCCATCCG 3240
 3181 TATGAGGCAAAATTAATTTTATATGCGGGGTGACACGACCGCCCTCCATCCG 3240
 3241 TGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3300
 3241 TGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3300
 3301 AGACCCATTTCTTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3360
 3301 AGACCCATTTCTTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3360
 3361 TATTATGATAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420
 3361 TATTATGATAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3420

3421 TGTAGCGCTTCTGAGCGCTGGGACCTAGGTTCAAGTTGGGCCCTCAAGAGGAGCCGTG 3480
 3421 TGTAGCGCTTCTGAGCGCTGGGACCTAGGTTCAAGTTGGGCCCTCAAGAGGAGCCGTG 3480
 3481 AGAATTGGGAAACTGCTTCTAGGAACTCTGGCTTCAACCCCTGCTCGGGCTGACCCCTT 3540
 3481 AGAATTGGGAAACTGCTTCTAGGAACTCTGGCTTCAACCCCTGCTCGGGCTGACCCCTT 3540
 3541 TCTGATCGTCTCGGCCCTGCTGATTGTTCCGATGGTCTCTCTCCCTCTCTCTTTTGTG 3600
 3541 TCTGATCGTCTCGGCCCTGCTGATTGTTCCGATGGTCTCTCTCCCTCTCTCTTTTGTG 3600
 3601 GCTCCGCTGTGCTCATCTGACCCGTTTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTG 3660
 3601 GCTCCGCTGTGCTCATCTGACCCGTTTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTG 3660
 3661 AATGCTCCAGCTGTGCTGCTGACTTCTGGGTTCTGGGTCGTTGGGACATGAGATTTTAT 3720
 3661 AATGCTCCAGCTGTGCTGCTGACTTCTGGGTTCTGGGTCGTTGGGACATGAGATTTTAT 3720
 3721 GTTGAAGTGAAGTGAAGGATCGTAAGATTTTACAACTCTGATCTCTTGAACAATCTCTG 3780
 3721 GTTGAAGTGAAGTGAAGGATCGTAAGATTTTACAACTCTGATCTCTTGAACAATCTCTG 3780
 3781 GGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3840
 3781 GGTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3840
 3841 TGAATCCGACACCCACCCATCCCAATGAATGATGATGATGATGATGATGATGATGATGAT 3900
 3841 TGAATCCGACACCCACCCATCCCAATGAATGATGATGATGATGATGATGATGATGATGAT 3900
 3901 TGCATCTGACCCCGGGGGTCTGGGACAGATTGGCAATGGGACCGTCCCTCTAAACC 3960
 3901 TGCATCTGACCCCGGGGGTCTGGGACAGATTGGCAATGGGACCGTCCCTCTAAACC 3960
 3961 TTGCCCCCTCGCCCTCGTTGCCAAATTAATAAGCTCTTAAAAACGCAAAAAAGGATTTA 4020
 3961 TTGCCCCCTCGCCCTCGTTGCCAAATTAATAAGCTCTTAAAAACGCAAAAAAGGATTTA 4020
 4021 AAAAA 4025
 4021 AAAAA 4025

RESULT 2

US-10-116-802-361
 ; Sequence 361, Application US/10116802
 ; Publication No. US20030065157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Amy Lasek
 ; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
 ; FILE REFERENCE: PA-0045 US
 ; CURRENT APPLICATION NUMBER: US/10/116,802
 ; CURRENT FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 60/281,593
 ; PRIOR FILING DATE: 2001-04-04
 ; NUMBER OF SEQ ID NOS: 519
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 361
 ; LENGTH: 4025
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 1136056.1
 US-10-116-802-361

Query Match 100.0%; Score 4025; DB 13; Length 4025;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

un on: April 21, 2004, 04:08:30 ; Search time 1593.74 Seconds
(without alignments)
11386.553 Million cell updates/sec

itle: US-10-002-600-46

erfect score: 4025

equences: 1 cattcataagactcagagct.....aaataaaaggatttaaaaaa 4025

coring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

earched: 2907579 seqs, 2254313464 residues

otal number of hits satisfying chosen parameters: 5815158

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| result No. | Score | Query Match | Length | ID | Description |
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| 1 | 4025 | 100.0 | 4025 | 10 | US-09-971-429B-15 |
| 2 | 4025 | 100.0 | 4025 | 13 | US-10-116-802-361 |
| 3 | 4025 | 100.0 | 4025 | 14 | US-10-002-600-46 |
| 4 | 1997 | 49.6 | 3851 | 15 | US-10-247-671-31 |
| 5 | 1982 | 49.2 | 3775 | 9 | US-09-954-456-2210 |
| 6 | 1982 | 49.2 | 3775 | 9 | US-09-880-107-2221 |
| 7 | 1982 | 49.2 | 3775 | 10 | US-09-960-706-649 |
| 8 | 1982 | 49.2 | 3775 | 10 | US-09-873-319-404 |
| 9 | 1982 | 49.2 | 3775 | 10 | US-09-873-367C-698 |
| 10 | 1982 | 49.2 | 3775 | 15 | US-10-205-823-133 |
| 11 | 1982 | 49.2 | 3775 | 15 | US-10-210-120-60 |
| 12 | 1982 | 49.2 | 3775 | 15 | US-10-004-113-27 |
| 13 | 1982 | 49.2 | 3775 | 16 | US-10-159-563-273 |
| 14 | 1982 | 49.2 | 3775 | 17 | US-10-394-948-11 |

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| 15 | 1965.4 | 48.8 | 3876 | 15 | US-10-198-846-12898 | Sequence 12898, A |
| 16 | 1700 | 42.2 | 3632 | 16 | US-10-144-194A-29 | Sequence 29, Appl |
| 17 | 1165 | 28.9 | 27184 | 15 | US-10-004-113-16 | Sequence 16, Appl |
| 18 | 1165 | 28.9 | 27184 | 17 | US-10-394-948-10 | Sequence 10, Appl |
| 19 | 797.4 | 19.8 | 1017 | 15 | US-10-004-113-18 | Sequence 18, Appl |
| 20 | 797.4 | 19.8 | 1017 | 17 | US-10-394-948-12 | Sequence 12, Appl |
| 21 | 796.2 | 19.8 | 4145 | 15 | US-10-004-113-14 | Sequence 14, Appl |
| 22 | 796.2 | 19.8 | 4145 | 17 | US-10-394-948-8 | Sequence 8, Appl |
| 23 | 657.2 | 16.3 | 1017 | 15 | US-10-004-113-15 | Sequence 15, Appl |
| 24 | 657.2 | 16.3 | 1017 | 17 | US-10-394-948-9 | Sequence 9, Appl |
| 25 | 401.4 | 10.0 | 561 | 15 | US-10-029-386-3791 | Sequence 13, Appl |
| 26 | 401.2 | 10.0 | 26993 | 15 | US-10-004-113-13 | Sequence 13, Appl |
| 27 | 401.2 | 10.0 | 26993 | 17 | US-10-394-948-7 | Sequence 7, Appl |
| 28 | 336.4 | 9.8 | 11176 | 9 | US-09-738-968-43 | Sequence 43, Appl |
| 29 | 366.8 | 9.1 | 1996 | 16 | US-10-144-194A-27 | Sequence 27, Appl |
| 30 | 339.4 | 8.4 | 459 | 15 | US-10-029-386-17491 | Sequence 17491, A |
| 31 | 334 | 8.3 | 888 | 15 | US-10-198-846-9406 | Sequence 9406, Ap |
| 32 | 279.2 | 6.9 | 2185 | 16 | US-10-108-260A-1814 | Sequence 1814, Ap |
| 33 | 272 | 6.8 | 7634 | 15 | US-10-311-455-2104 | Sequence 2104, Ap |
| 34 | 243 | 6.0 | 622 | 13 | US-10-027-632-23256 | Sequence 23256, A |
| 35 | 243 | 6.0 | 622 | 16 | US-10-027-632-23256 | Sequence 23256, A |
| 36 | 230 | 5.7 | 691 | 13 | US-10-027-632-106560 | Sequence 106560, |
| 37 | 230 | 5.7 | 691 | 16 | US-10-027-632-106560 | Sequence 106560, |
| 38 | 226 | 5.6 | 7634 | 15 | US-10-311-455-2103 | Sequence 2103, Ap |
| 39 | 224.2 | 5.6 | 655 | 15 | US-10-198-846-13313 | Sequence 13313, A |
| 40 | 148.6 | 3.7 | 389 | 10 | US-09-918-995-8755 | Sequence 8755, Ap |
| 41 | 129.4 | 3.2 | 341 | 9 | US-09-604-287A-440 | Sequence 440, App |
| 42 | 129.4 | 3.2 | 341 | 10 | US-09-551-621-440 | Sequence 440, App |
| 43 | 129.4 | 3.2 | 341 | 14 | US-10-007-805-440 | Sequence 440, App |
| 44 | 129.4 | 3.2 | 341 | 15 | US-10-076-622-440 | Sequence 440, App |
| 45 | 129.4 | 3.2 | 341 | 15 | US-10-124-805-440 | Sequence 440, App |

ALIGNMENTS

RESULT 1
US-09-971-429B-15
; Sequence 15, Application US/0971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shylan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971.429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 1136056.1
US-09-971-429B-15

| | | | | |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match | 100.0% | Score 4025; | DB 10; | Length 4025; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 4025; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | CATTCTAAGACTCAGAGCTACGCCACCGGACACCGGACACCGGACCAAGACTTGAAA | 60 | |
| DB | 1 | CATTCTAAGACTCAGAGCTACGCCACCGGACACCGGACACCGGACCAAGACTTGAAA | 60 | |
| QY | 61 | CTTGATTGTTGGTCTCTTGGGGGTATGAATTTCAATCTTTTTTTTCCGG | 120 | |
| DB | 61 | CTTGATTGTTGGTCTCTTGGGGGTATGAATTTCAATCTTTTTTTTCCGG | 120 | |

